

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lal, Preeti  
Guegler, Karl J.  
Corley, Neil C.

(ii) TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
(B) STREET: 3174 PORTER DRIVE  
(C) CITY: PALO ALTO  
(D) STATE: CALIFORNIA  
(E) COUNTRY: USA  
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned  
(B) FILING DATE: Herewith  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: CERRONE, MICHAEL C.  
(B) REGISTRATION NUMBER: 39,132  
(C) REFERENCE/DOCKET NUMBER: PF-0527 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650) 855-0555  
(B) TELEFAX: (650) 845-4166

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vi) IMMEDIATE SOURCE:

(A) LIBRARY: PROSTUT10  
(B) CLONE: 1691243

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 :

Met	Val	His	Val	Ala	Tyr	Ser	Leu	Cys	Leu	Pro	Met	Arg	Arg	Ser
5							10						15	
Glu	Arg	Tyr	Leu	Phe	Leu	Asn	Met	Ala	Tyr	Gln	Gln	Val	His	Ala
20							25						30	
Asn	Ile	Glu	Asn	Ser	Trp	Asn	Glu	Glu	Glu	Val	Trp	Arg	Ile	Glu
35							40						45	
Met	Tyr	Ile	Ser	Phe	Gly	Ile	Met	Ser	Leu	Gly	Leu	Leu	Ser	Leu
50							55						60	
Leu	Ala	Val	Thr	Ser	Ile	Pro	Ser	Val	Ser	Asn	Ala	Leu	Asn	Trp
65							70						75	
Arg	Glu	Phe	Ser	Phe	Ile	Gln	Ser	Thr	Leu	Gly	Tyr	Val	Ala	Leu
80							85						90	
Leu	Ile	Ser	Thr	Phe	His	Val	Leu	Ile	Tyr	Gly	Trp	Lys	Arg	Ala
95							100						105	
Phe	Glu	Glu	Tyr	Tyr	Arg	Phe	Tyr	Thr	Pro	Pro	Asn	Phe	Val	
110							115						120	
Leu	Ala	Leu	Val	Leu	Pro	Ser	Ile	Val	Ile	Leu	Asp	Leu	Leu	Gln
125							130						135	
Leu	Cys	Arg	Tyr	Pro	Asp									
140														

## (2) INFORMATION FOR SEQ ID NO: 2 :

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT03
- (B) CLONE: 1999442

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2 :

Met	Phe	Leu	Pro	Pro	Val	Val	Leu	Ala	Ile	Arg	Ser	Arg	Tyr	Val
5							10						15	
Leu	Glu	Ala	Ala	Val	Tyr	Thr	Phe	Thr	Met	Phe	Phe	Ser	Thr	Phe
20							25						30	
Tyr	His	Ala	Cys	Asp	Gln	Pro	Gly	Ile	Val	Val	Phe	Cys	Ile	Met
35							40						45	
Asp	Tyr	Asp	Val	Leu	Gln	Phe	Cys	Asp	Phe	Leu	Gly	Ser	Leu	Met
50							55						60	
Ser	Val	Trp	Val	Thr	Val	Ile	Ala	Met	Ala	Arg	Leu	Gln	Pro	Val
65							70						75	
Val	Lys	Gln	Val	Leu	Tyr	Leu	Leu	Gly	Ala	Met	Leu	Leu	Ser	Met
80							85						90	
Ala	Leu	Gln	Leu	Asp	Arg	His	Gly	Leu	Trp	Asn	Leu	Leu	Gly	Pro
95							100						105	
Ser	Leu	Phe	Ala	Leu	Gly	Ile	Leu	Ala	Thr	Ala	Trp	Thr	Val	Arg
110							115						120	
Ser	Val	Arg	Arg	Arg	His	Cys	Tyr	Pro	Pro	Thr	Trp	Arg	Arg	Trp
125							130						135	
Leu	Phe	Tyr	Leu	Cys	Pro	Gly	Ser	Leu	Ile	Ala	Gly	Ser	Ala	Val
140							145						150	
Leu	Leu	Tyr	Ala	Phe	Val	Glu	Thr	Arg	Asp	Asn	Tyr	Phe	Tyr	Ile

155	160	165
His Ser Ile Trp His Met Leu Ile Ala	Gly Ser Val Gly Phe Leu	
170	175	180
Leu Pro Pro Arg Ala Lys Thr Asp His	Gly Val Pro Ser Gly Ala	
185	190	195
Arg Ala Arg Gly Cys Gly Tyr Gln Leu	Cys Ile Asn Glu Gln Glu	
200	205	210
Glu Pro Gly Pro Arg Gly Pro Arg Arg	Gly His Cys Gln Gln His	
215	220	225
Leu Cys Gln Leu Arg Gly Ala Leu Gly	Leu Ala Leu Arg Gly Tyr	
230	235	240
Glu Cys Phe Leu Glu Phe Leu Gly	Val Trp Ser Pro Leu Arg	
245	250	255
Arg Arg Gln Ala Val Phe Leu Glu Asp	Met Glu Ser Phe Ser Arg	
260	265	270
Thr Gln Asn Ser Ser Arg Asp Leu Glu	Pro Phe Pro Gly His Gly	
275	280	285
Glu Leu Pro Glu Gly Leu Glu Ser Pro	Cys Ile Met Glu Ser Phe	
290	295	300
Leu Arg Thr Gly Ala Tyr Ala Gly Thr	Glu Ser Leu Arg Thr Lys	
305	310	315
Glu Ser Leu Leu Gln Val Trp Ser Leu	Ser Trp Asp Ala Glu Pro	
320	325	330
Ser Gln Asp Met Asp Ser Phe Pro Gly	Arg Gln Ser Pro Val Arg	
335	340	345
Ser Thr Ala Ser Phe Gln Arg Arg Trp	Ser Leu Ser Trp Gly Asn	
350	355	360
Gln Ile Ser Arg Phe Ser Gln Arg Leu	Ser Asn Ser Gly Leu Arg	
365	370	375
Leu Pro Ser Gln Arg Gln Arg Leu Gly	Cys Ala Val Leu Trp Arg	
380	385	390
Arg Asp Cys Arg Met Asp Gly Ala Gly	Thr Gly Ala Val Trp Val	
395	400	405
Ala Gly Ile Leu Val		
410		

## (2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1213 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: PROSTUT10
  - (B) CLONE: 1691243

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3 :

CAAGTATAAGG AGATTTCAC	CTTGGTTGGA AACCTGGTTA CAGTGTAGAA AACAGCTTGG	60
ATTACTAAGT TTTTCTTCG	CTATGGCCA TGTGCGCTAC AGCCTCTGCT TACCGATGAG	120
AAGGTCAAGAG AGATATTGT	TTCTCAACAT GGCTTATCAG CAGGTTCATG CAAATATTGA	180
AAACTCTTGG AATGAGGAAG	AAGTTTGAG AATGAAATG TATATCTCCT TTGGCATAAT	240
GAGCCTTGGC TTACTTTCCC	TCCTGGCAGT CACTTCTATC CCTTCAGTGA GCAATGCTTT	300
AAACTGGAGA GAATTCAAGTT	TTATTCAGTC TACACTTGGAA TATGTCGCTC TGCTCATAAG	360
TACTTTCCAT GTTTAATTT	ATGGATGGAA ACGAGCTTTT GAGGAAGAGT ACTACAGATT	420
TTATACACCA CCAAACCTTG	TTCTTGCTCT TGTTTGCCC TCAATTGTAA TTCTGGATCT	480

TTTGCAGCTT TGCAGATACC CAGACTGAGC TGGAACTGGA ATTTGTCTTC CTATTGACTC 540  
 TACTTCTTAA AAAGCGGCTG CCCATTACAT TCCTCAGCTG TCCTTGCAGT TAGGTGTACA 600  
 TGTGACTGAG TGTTGGCCAG TGAGATGAAG TCTCCTCAAA GGAAGGCAGC ATGTGTCCCT 660  
 TTTCATCCCT TCATCTTGCT GCTGGGATTG TGGATATAAC AGGAGCCCTG GCAGCTGTCT 720  
 CCAGAGGATC AAAGCCACAC CCAAAGAGTA AGGCAGATTAGAGACAGAA AGACCTTGAC 780  
 TACTTCCCTA CTTCCACTGC TTTTCCCTGC ATTTAAGCCA TTGTAATCT GGGTGTGTTA 840  
 CATGAAGTGA AAATTAATTC TTTCTGCCCT TCAGTTCTT ATCCTGATAC CATTAAACAC 900  
 TGTCTGAATT AACTAGACTG CAATAATTCT TTCTTTGAA AGCTTTAAA GGATAATGTG 960  
 CAATTCACTA TAAAATTGAT TTTCCATTGT CAATTAGTTA TACTCATTCT CCTGCCTTGA 1020  
 TCTTTCATTA GATATTTTGT ATCTGCTTGG AATATATTAT CTTCTTTTA ACTGTGTAAT 1080  
 TGGTAATTAC TAAAACCTCG TAATCTCCAA AATATTGCTA TCAAATTACA CACCATGTTT 1140  
 TCTATCATTC TCATAGATCT GCCTTATAAAA CATTAAATA AAAAGTACTA TTTAATGATT 1200  
 TAAAAAAA AAA 1213

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1297 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: BRSTTUT03  
 (B) CLONE: 1999442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4 :

CGGACGGCTG GGCTGCTCTG CCTGAGCAAC CTCATGTTTC TGCCACCTGT GGTCTGGCC 60  
 ATTGGGAGCT GATATGTGCT GGAAGCTGCA GTCTACACCT TCACCAGTGT CTTCTCCACG 120  
 TTCTATCATG CCTGTGACCA GCCAGGCATC GTGGTTTCT GCATCATGGA CTACGATGTG 180  
 CTGAGTTCT GTGATTTCTT GGGCTCTTA ATGTCCTGTG GGGTCATGT CATTGCCATG 240  
 GCTCGTTTAC AGCCCGTGGT CAAGCAGGTG CTGTATTGTC TGGGAGCTAT GCTGCTGTCC 300  
 ATGGCTCTGC AGCTTGACCG ACATGGACTC TGGAACCTGC TTGGACCCAG TCTCTCGCC 360  
 CTGGGGATCT TGGCCACAGC CTGGACAGTA CGCAGCGTCC GCCGCCGGCA CTGCTACCCA 420  
 CCCACGTGGC GCCGCTGGCT TTTCTACTTG TGCCCTGGCA GCCTTATTGTC AGGCAGTGCC 480  
 GTCCTGCTT ATGCTTTGT GGAGACCCGG GACAACACT TCTACATTCA CAGCATTGG 540  
 CATATGCTCA TTGGGGCAG TGTGGCTTC CTGCTGCCCT CTCGTGCCAA GACTGACCCAC 600  
 GGGGTCCCCT CTGGAGCCCG GGCCCGGGC TGTGGTTACC AGCTATGCAT CAACGAGCAG 660  
 GAGGAGCCTG GGCCTCGTGG GCCCAGGAGG GGCCACTGTC AGCAGCATCT GTGCCAGCTG 720  
 AGAGGGGCTT TGGGCTGGC CCTGAGGGGA TATGAATGCT TCCTAGAGTT CTTTCTGGGG 780  
 GTGTGGAGCC CTCTAGAAG GAGACAGGCT GTATTCTTG AGGACATGGA GTCTTCTCA 840  
 AGGACACAAA ACTCTTCCAG GGACCTGGAG CCCTTCCAG GACATGGAGA ACTTCCTGAG 900  
 GGCCTGGAGT CCCCCCTGCAT CATGGAGTCC TTCTTAAGGA CTGGAGCCTA TGCAGGCACA 960  
 GAGTCCCTCA GGACCAAGGA GTCCCTCCTG CAGGTGTGGA GCCTTCCTG GGATGCAGAG 1020  
 CCTTCCCAAG ACATGGATTG CTTCCCAGGG AGACAAAGCC CTGTCAGGAG CACAGCATCT 1080  
 TTCCAGAGGA GGTGGAGTCT ATCTTGGGG AACCAAATT CCAGATTTTC CCAGAGGCTC 1140  
 AGCAACTCTG GCCTCAGGCT TCCTTCCAG AGGCAGCGTC TGGGCTGTGC TGTGCTGTGG 1200  
 AGGAGGGATT GCAGGATGGA TGGAGCTGG ACTGGGGCTG TCTGGGTGGC TGGTATCCTC 1260  
 GTTTGATACA GGTGGAGTCT CTGTGTCTCC ATAGAAG 1297

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 76 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: GenBank  
 (B) CLONE: 1216498

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5 :

Met	Gly	Arg	Ala	Met	Val	Val	Arg	Leu	Gly	Leu	Leu	Leu	
					5			10				15	
Leu	Ala	Leu	Leu	Leu	Pro	Thr	Gln	Ile	Tyr	Cys	Asn	Gln	Thr
					20			25				30	
Val	Ala	Pro	Phe	Ser	Gly	Asn	Gln	Ser	Ile	Ser	Ala	Ala	Pro
					35			40				45	
Pro	Thr	Asn	Ala	Thr	Thr	Arg	Ser	Gly	Cys	Ser	Ser	Leu	Gln
					50			55				60	
Thr	Ala	Gly	Leu	Leu	Ala	Leu	Ser	Leu	Ser	Leu	Leu	His	Leu
					65			70				75	
Cys													

## (2) INFORMATION FOR SEQ ID NO: 6 :

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 261 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: GenBank  
 (B) CLONE: 130989

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6 :

Met	Trp	Val	Pro	Val	Val	Phe	Leu	Thr	Leu	Ser	Val	Thr	Trp	Ile	
						5			10				15		
Gly	Ala	Ala	Pro	Leu	Ile	Leu	Ser	Arg	Ile	Val	Gly	Gly	Trp	Glu	
					20			25				30			
Cys	Glu	Lys	His	Ser	Gln	Pro	Trp	Gln	Val	Leu	Val	Ala	Ser	Arg	
					35			40				45			
Gly	Arg	Ala	Val	Cys	Gly	Gly	Val	Leu	Val	His	Pro	Gln	Trp	Val	
					50			55				60			
Leu	Thr	Ala	Ala	His	Cys	Ile	Arg	Asn	Lys	Ser	Val	Ile	Leu	Leu	
					65			70				75			
Gly	Arg	His	Ser	Leu	Phe	His	Pro	Glu	Asp	Thr	Gly	Gln	Val	Phe	
					80			85				90			
Gln	Val	Ser	His	Ser	Phe	Pro	His	Pro	Leu	Tyr	Asp	Met	Ser	Leu	
					95			100				105			
Leu	Lys	Asn	Arg	Phe	Leu	Arg	Pro	Gly	Asp	Asp	Ser	Ser	His	Asp	
					110			115				120			
Leu	Met	Leu	Leu	Arg	Leu	Ser	Glu	Pro	Ala	Glu	Leu	Thr	Asp	Ala	
					125			130				135			
Val	Lys	Val	Met	Asp	Leu	Pro	Thr	Gln	Glu	Pro	Ala	Leu	Gly	Thr	
					140			145				150			
Thr	Cys	Tyr	Ala	Ser	Gly	Trp	Gly	Ser	Ile	Glu	Pro	Glu	Glu	Phe	
					155			160				165			
Leu	Thr	Pro	Lys	Lys	Leu	Gln	Cys	Val	Asp	Leu	His	Val	Ile	Ser	
					170			175				180			
Asn	Asp	Val	Cys	Ala	Gln	Val	His	Pro	Gln	Lys	Val	Thr	Lys	Phe	
					185			190				195			

Met Leu Cys Ala Gly Arg Trp Thr Gly Gly Lys Ser Thr Cys Ser  
 200 205 210  
 Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gly Val Leu Gln Gly  
 215 220 225  
 Ile Thr Ser Trp Gly Ser Glu Pro Cys Ala Leu Pro Glu Arg Pro  
 230 235 240  
 Ser Leu Tyr Thr Lys Val Val His Tyr Arg Lys Trp Ile Lys Asp  
 245 250 255  
 Thr Ile Val Ala Asn Pro  
 260

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 2459993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7 :

Met Leu Ala Cys Leu Cys Cys Lys Lys Gly Gly Ile Gly Phe Lys  
 5 10 15  
 Glu Phe Glu Asn Ala Glu Gly Asp Glu Tyr Val Ala Asp Phe Ser  
 20 25 30  
 Glu Gln Gly Ser Pro Ala Ala Ala Ala Gln Thr Gly Pro Asp Val  
 35 40 45  
 Tyr Val Leu Pro Leu Thr Glu Val Ser Leu Pro Met Ala Lys Gln  
 50 55 60  
 Pro Gly Arg Ser Val Gln Leu Leu Lys Ser Thr Asp Leu Gly Arg  
 65 70 75  
 His Ser Leu Leu Tyr Leu Lys Glu Ile Gly His Gly Trp Phe Gly  
 80 85 90  
 Lys Val Phe Leu Gly Glu Val His Ser Gly Val Ser Gly Thr Gln  
 95 100 105  
 Val Val Val Lys Glu Leu Lys Val Ser Ala Ser Val Gln Glu Gln  
 110 115 120  
 Met Gln Phe Leu Glu Glu Ala Gln Pro Tyr Arg Ala Leu Gln His  
 125 130 135  
 Ser Asn Leu Leu Gln Cys Leu Ala Gln Cys Ala Glu Val Thr Pro  
 140 145 150  
 Tyr Leu Leu Val Met Glu Phe Cys Pro Leu Gly Asp Leu Lys Gly  
 155 160 165  
 Tyr Leu Arg Ser Cys Arg Val Thr Glu Ser Met Ala Pro Asp Pro  
 170 175 180  
 Leu Thr Leu Gln Arg Met Ala Cys Glu Val Ala Cys Gly Val Leu  
 185 190 195  
 His Leu His Arg His Asn Tyr Val His Ser Asp Leu Ala Leu Arg  
 200 205 210  
 Asn Cys Leu Leu Thr Ala Asp Leu Thr Val Lys Val Gly Asp Tyr  
 215 220 225  
 Gly Leu Ser His Cys Lys Tyr Arg Glu Asp Tyr Leu Val Thr Ala  
 230 235 240  
 Asp Gln Leu Trp Val Pro Leu Arg Trp Ile Ala Pro Glu Leu Val

245 250 255  
 Asp Glu Val His Gly Asn Leu Leu Val Val Asp Gln Thr Lys Ser  
 260 265 270  
 Ser Asn Val Trp Ser Leu Gly Val Thr Ile Trp Glu Leu Phe Glu  
 275 280 285  
 Leu Gly Ala Gln Pro Tyr Pro Gln His Ser Asp Arg Gln Val Leu  
 290 295 300  
 Ala Tyr Ala Val Arg Glu Gln Gln Leu Lys Leu Pro Lys Pro Gln  
 305 310 315  
 Leu Gln Leu Ala Leu Ser Asp Arg Trp Tyr Glu Val Met Gln Phe  
 320 325 330  
 Cys Trp Leu Gln Pro Glu Gln Arg Pro Thr Ala Glu Glu Val His  
 335 340 345  
 Leu Leu Leu Ser Tyr Leu Cys Ala Lys Gly Thr Thr Glu Leu Glu  
 350 355 360  
 Glu Glu Phe Glu Arg Arg Trp Arg Ser Leu Arg Pro Gly Gly Ser  
 365 370 375  
 Thr Gly Leu Gly Ser Gly Ser Ala Ala Pro Ala Ala Ala Thr Ala  
 380 385 390  
 Ala Ser Ala Glu Leu Thr Ala Ala Ser Ser Phe Pro Leu Leu Glu  
 395 400 405  
 Arg Phe Thr Ser Asp Gly Phe His Val Asp Ser Asp Asp Val Leu  
 410 415 420  
 Thr Val Thr Glu Thr Ser His Gly Leu Asn Phe Glu Tyr Lys Trp  
 425 430 435  
 Glu Ala Gly Cys Gly Ala Glu Glu Tyr Pro Pro Ser Gly Ala Ala  
 440 445 450  
 Ser Ser Pro Gly Ser Ala Ala Arg Leu Gln Glu Leu Cys Ala Pro  
 455 460 465  
 Asp Ser Ser Pro Pro Gly Val Val Pro Val Leu Ser Ala His Ser  
 470 475 480  
 Pro Ser Val Gly Ser Glu Tyr Phe Ile Arg Leu Glu Gly Ala Val  
 485 490 495  
 Pro Ala Ala Gly His Asp Pro Asp Cys Ala Gly Cys Ala Pro Ser  
 500 505 510  
 Pro Gln Ala Val Thr Asp Gln Asp Asn Asn Ser Glu Glu Ser Thr  
 515 520 525  
 Val Ala Ser Leu Ala Met Glu Pro Leu Leu Gly His Ala Pro Pro  
 530 535 540  
 Thr Glu Gly Leu Trp Gly Pro Cys Asp His His Ser His Arg Arg  
 545 550 555  
 Gln Gly Ser Pro Cys Pro Ser Arg Ser Pro Ser Pro Gly Thr Pro  
 560 565 570  
 Met Leu Pro Ala Glu Asp Ile Asp Trp Gly Val Ala Thr Phe Cys  
 575 580 585  
 Pro Pro Phe Phe Asp Asp Pro Leu Gly Ala Ser Pro Ser Gly Ser  
 590 595 600  
 Pro Gly Ala Gln Pro Ser Pro Ser Asp Glu Glu Pro Glu Glu Gly  
 605 610 615  
 Lys Val Gly Leu Ala Ala Gln Cys Gly His Trp Ser Ser Asn Met  
 620 625 630  
 Ser Ala Asn Asn Asn Ser Ala Ser Arg Asp Pro Glu Ser Trp Asp  
 635 640 645  
 Pro Gly Tyr Val Ser Ser Phe Thr Asp Ser Tyr Arg Asp Asp Cys  
 650 655 660  
 Ser Ser Leu Glu Gln Thr Pro Arg Ala Ser Pro Glu Val Gly His  
 665 670 675  
 Leu Leu Ser Gln Glu Asp Pro Arg Asp Phe Leu Pro Gly Leu Val  
 680 685 690  
 Ala Val Ser Pro Gly Gln Glu Pro Ser Arg Pro Phe Asn Leu Leu  
 695 700 705

Pro Leu Cys Pro Ala Lys Gly Leu Ala Pro Ala Ala Cys Leu Ile  
 710 715 720  
 Thr Ser Pro Trp Thr Glu Gly Ala Val Gly Gly Ala Glu Asn Pro  
 725 730 735  
 Ile Val Glu Pro Lys Leu Ala Gln Glu Ala Glu Gly Ser Ala Glu  
 740 745 750  
 Pro Gln Leu Pro Leu Pro Ser Val Pro Ser Pro Ser Cys Glu Gly  
 755 760 765  
 Ala Ser Leu Pro Ser Glu Glu Ala Ser Ala Pro Asp Ile Leu Pro  
 770 775 780  
 Ala Ser Pro Thr Pro Ala Ala Gly Ser Trp Val Thr Val Pro Glu  
 785 790 795  
 Pro Ala Pro Thr Leu Glu Ser Ser Gly Ser Ser Leu Gly Gln Glu  
 800 805 810  
 Ala Pro Ser Ser Glu Asp Glu Asp Thr Thr Glu Ala Thr Ser Gly  
 815 820 825  
 Val Phe Thr Asp Leu Ser Ser Asp Gly Pro His Thr Glu Lys Ser  
 830 835 840  
 Gly Ile Val Pro Ala Leu Arg Ser Leu Gln Lys Gln Val Gly Thr  
 845 850 855  
 Pro Asp Ser Leu Asp Ser Leu Asp Ile Pro Ser Ser Ala Ser Asp  
 860 865 870  
 Gly Gly Cys Glu Val Leu Ser Pro Ser Ala Ala Gly Pro Pro Gly  
 875 880 885  
 Gly Gln Pro Arg Ala Val Asp Ser Gly Tyr Asp Thr Glu Asn Tyr  
 890 895 900  
 Glu Ser Pro Glu Phe Val Leu Lys Glu Ala His Glu Ser Ser Glu  
 905 910 915  
 Pro Glu Ala Phe Gly Glu Pro Ala Ser Glu Gly Glu Ser Pro Gly  
 920 925 930  
 Pro Asp Pro Leu Leu Ser Val Ser Leu Gly Gly Leu Ser Lys Lys  
 935 940 945  
 Ser Pro Tyr Arg Asp Ser Ala Tyr Phe Ser Asp Leu Asp Ala Glu  
 950 955 960  
 Ser Glu Pro Thr Phe Gly Pro Glu Lys His Ser Gly Ile Gln Asp  
 965 970 975  
 Ser Gln Lys Glu Gln Asp Leu Arg Ser Pro Pro Ser Pro Gly His  
 980 985 990  
 Gln Ser Val Gln Ala Phe Pro Arg Ser Ala Val Ser Ser Glu Val  
 995 1000 1005  
 Leu Ser Pro Pro Gln Gln Ser Glu Glu Pro Leu Pro Glu Val Pro  
 1010 1015 1020  
 Arg Pro Glu Pro Leu Gly Ala Gln Gly Pro Val Gly Val Gln Pro  
 1025 1030 1035  
 Val Pro Gly Pro Ser His Ser Lys Cys Phe Pro Leu Thr Ser Val  
 1040 1045 1050  
 Pro Leu Ile Ser Glu Gly Ser Gly Thr Glu Pro Gln Gly Pro Ser  
 1055 1060 1065  
 Gly Gln Leu Ser Gly Arg Ala Gln Gln Gly Gln Met Gly Asn Pro  
 1070 1075 1080  
 Ser Thr Pro Arg Ser Pro Leu Cys Leu Ala Leu Pro Gly His Pro  
 1085 1090 1095  
 Gly Ala Leu Glu Gly Arg Pro Glu Glu Asp Glu Asp Thr Glu Asp  
 1100 1105 1110  
 Ser Glu Glu Ser Asp Glu Glu Leu Arg Cys Tyr Ser Val Gln Glu  
 1115 1120 1125  
 Pro Ser Glu Asp Ser Glu Glu Glu Pro Pro Ala Val Pro Val Val  
 1130 1135 1140  
 Val Ala Glu Ser Gln Ser Ala Arg Asn Leu Arg Ser Leu Leu Lys  
 1145 1150 1155  
 Met Pro Ser Leu Leu Ser Glu Ala Phe Cys Asp Asp Leu Glu Arg

1160	1165	1170
Lys Lys Lys Ala Val Ser Phe Phe Asp Asp Val Thr Val Tyr Leu		
1175	1180	1185
Phe Asp Gln Glu Ser Pro Thr Arg Glu Thr Gly Glu Pro Phe Pro		
1190	1195	1200
Ser Thr Lys Glu Ser Leu Pro Thr Phe Leu Glu Gly Gly Pro Ser		
1205	1210	1215
Ser Pro Ser Ala Thr Gly Leu Pro Leu Arg Ala Gly His Ser Pro		
1220	1225	1230
Asp Ser Ser Ala Pro Glu Pro Gly Ser Arg Phe Glu Trp Asp Gly		
1235	1240	1245
Asp Phe Pro Leu Val Pro Gly Lys Ala Ala Leu Val Thr Glu Leu		
1250	1255	1260
Asp Pro Ala Asp Pro Val Leu Ala Ala Pro Pro Thr Pro Ala Ala		
1265	1270	1275
Pro Phe Ser Arg Phe Thr Val Ser Pro Thr Pro Ala Ser Arg Phe		
1280	1285	1290
Ser Ile Thr His Ile Ser Asp Ser Asp Ala Gln Ser Val Gly Gly		
1295	1300	1305
Pro Ala Ala Gly Ala Gly Gly Arg Tyr Thr Glu Ala		
1310	1315	